pGN1

```
  TaqI                                                         HindIII
  |                                                            | AluI           TaqI
  |                                                            | |              |
1 GTCGAGGCAGTCACTAACATGAAGTTTGACGAGGAGCCCAACTATGGGAAGCTTATTTCTCTTTTCGAT   69
  3                                                              52             66
                                                               50

                                                               SacI
            HhaI   XbaI                                       AluI
            |      |                                          | |
70 ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAATTGATGGAGCTCTAAAGGTTGCTGGCTGT   138
            89     95                                         119
                                                                121

     NdeI                                                               NdeI
     |                                                                  |
139 TTTCTTGTTCATATGATTAACTTCTAAACTTGTGTATAAATATTCTCTGAAAGTGCTTCTTTTGGCATA   207
     150                                                                206

208 TGTAGGTTGGGCAAAAACGAGGAAGATTGCTTCTCAATTTGGAAGATGATGAACAGCCGAAGAAGAAAA   276

                           Sau3AI
                              DdeI
                           |  |
277 TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAACGGTCGTCGTCCCATGAAACAGAGGT   345
                              309
                           305
```

FIG. 1A

```
EcoRV
                                                                             |
346 AACACATTTTTGCATATACACTTTGATAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA  414
                                                                              408

                          NaeI
                         MspI
                         HpaII
                    AluI HhaI                                  HaeIII      AluI
                    |    |||                                   |           |
415 CAATGTTGGAGAGACAANGCTGCGCJRRCATATACAGAAGGGAAATGAAGATGGCCTTTTGATTAGCTG  483
                    434  439                                   469         481
                          440
                          440
                           441

               AluI                                         HinfI
               |                                            |
484 TGTAGCATCAGCAGCTAATCTCTGGGCTCTCATCATGGATGCTGGAACTGGATTCACTTCTCAAGTTTA  552
               498                                          535

            MspI
            HpaII                                             HinfI
            |                                                 |
553 TGAGTTGTCACCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAATCAATCTGATTTGT  621
            564                                               606
            564

        DdeI
        |
622 AGTAAACTAAGAAGAACTTACCTTATGATTTCCCCGCAGGACTGGATTATGGAACAATGGGAAAAGAAC  690
        629
```

FIG. 1B

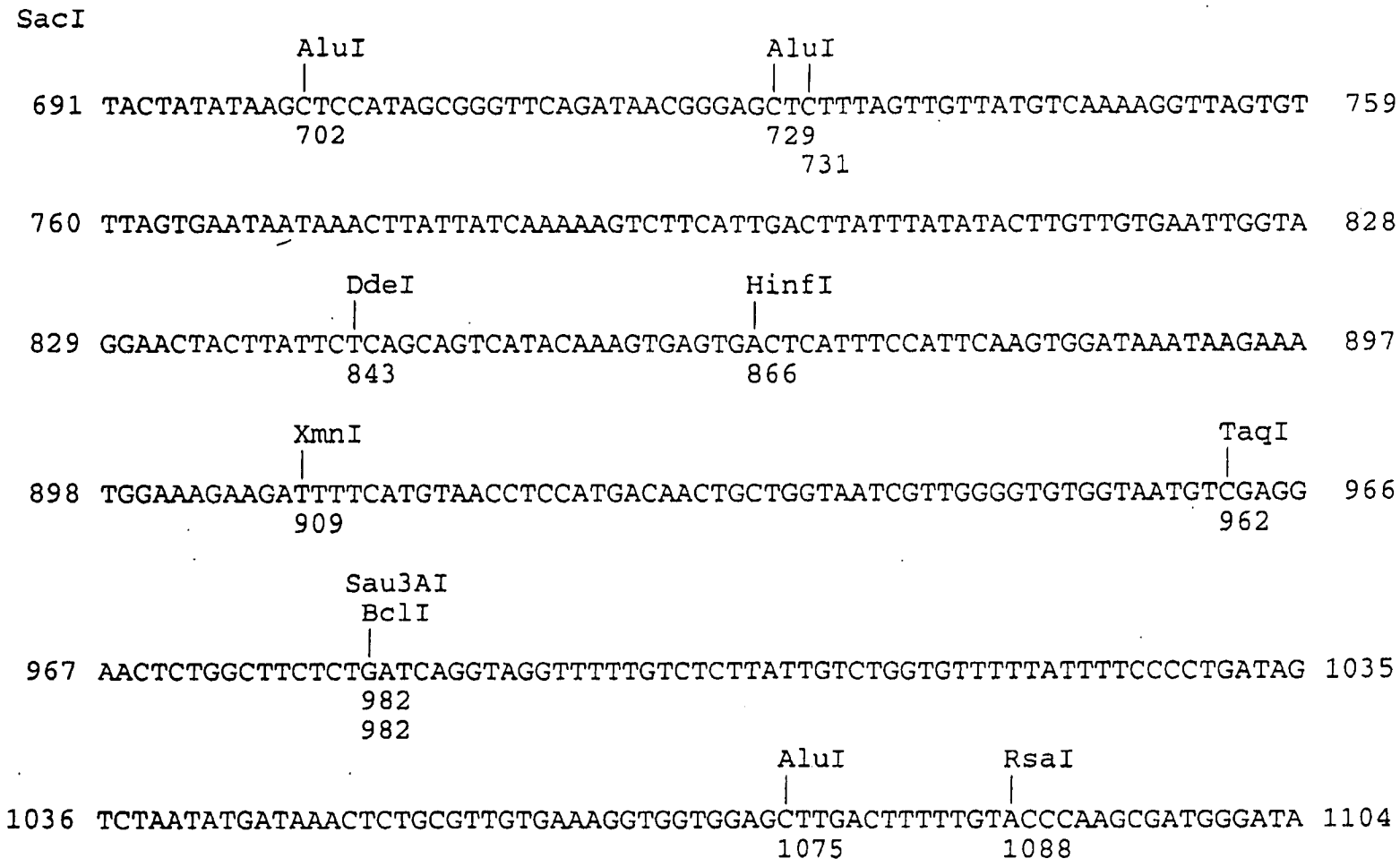

FIG. 1C

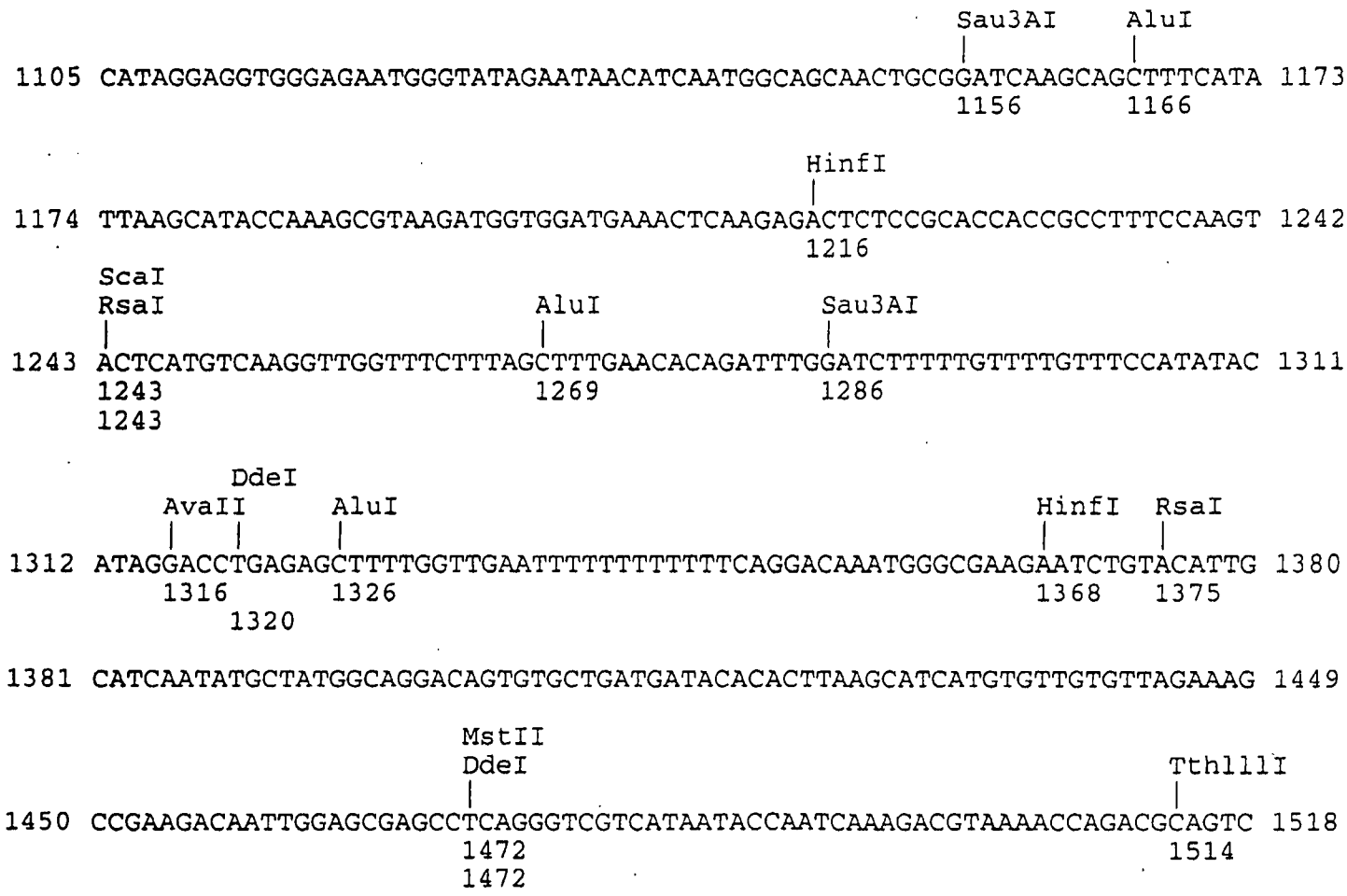

FIG. 1D

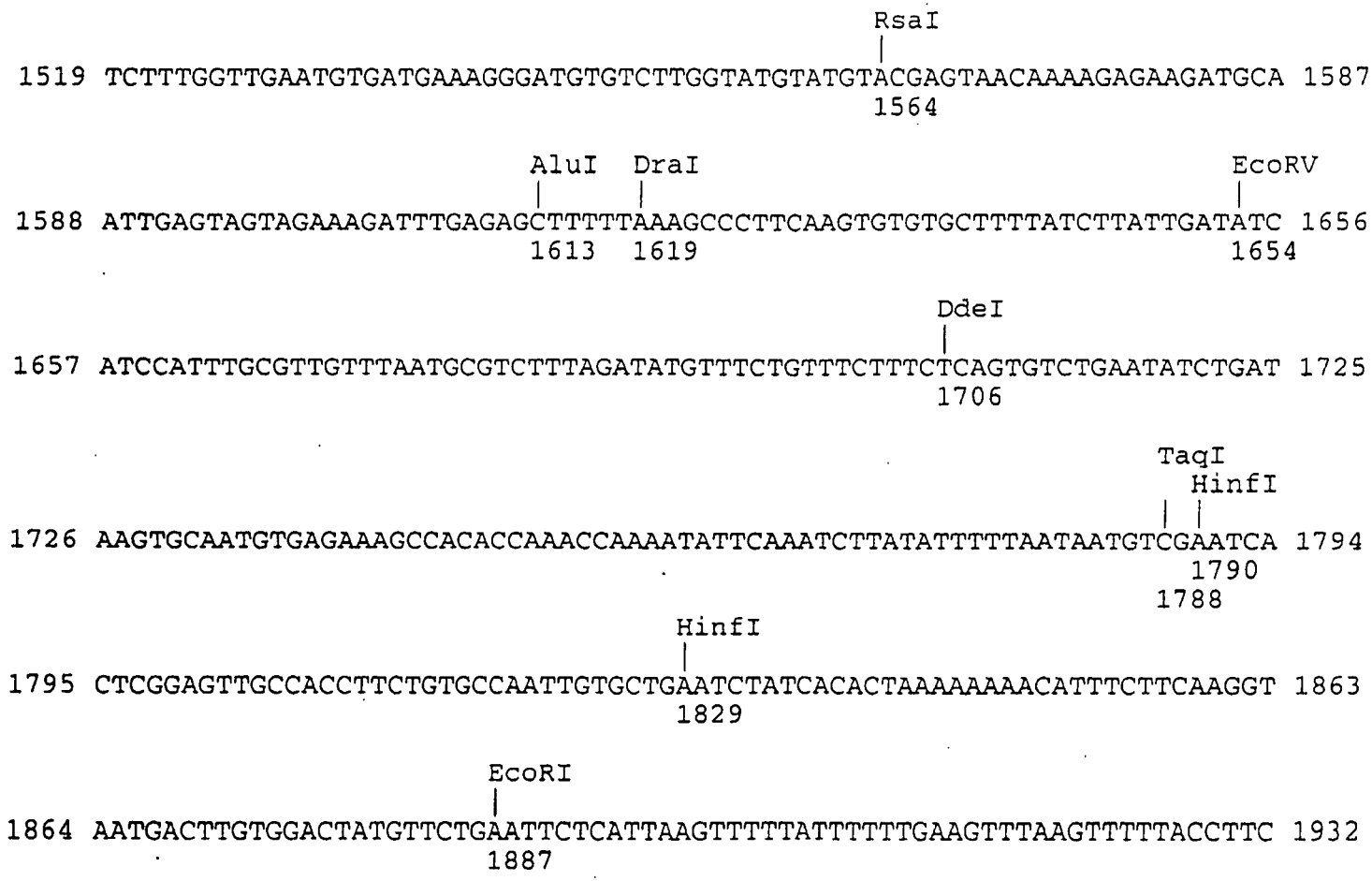

FIG. 1E

```
                                                 BstNI     AluI                   SphI
                                                 |         |                      |
1933 TTTTTTGAAAAATATCGTTCATAAGATGTCACGCCAGGACATGAGCTACACATCACATATTAGCATGCA 2001
                                                 1968      1978                   2000

                                               AluI                     NdeI
                                               |                        |
2002 GATGCGGACGATTTGTCACTCACTTCAAACACCTAAAAGAGCTTCTCTCACAGCACACACACATATG 2070
                                               2043                     2067

       SphI
     NsiI
     | |            Sau3AI
     | |            |
2071 CATGCAATATTTACACGTGATCGCCATGCAAATCTCCATTCTCACCTATAAATTAGAGGCTCGGCTTCA 2139
     2073           2089
       2075

                                                                AluI
                                                                |
2140 CTTTTTACTCAAACCAAAACTCATCACTACAAAACATACACAAATGGCGAACAAGCTCTTC 2200
                                                  Met           2195
```

FIG. 1F

Lambda CGNI-2

NCG-I86 Linear   Length = 4325

```
 XhoI
  TaqI                                           HindIII
 AvaI                                              AluI          TaqI
 ||                                              | |             |
CTCGAGGCAGTCACTAACATGAAGTTTGACGAGGAGCCCAACTATGGAAGCTTATTTCTCTTTTCGAT    69
 2                                                 52            66
  3                                              50

                                                  SacI
                   HhaI  XbaI                    AluI
                   |     |                       | |
ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAATTGATGGAGCTCTAAAGGTTGCTGGCTGT   138
                   89    95                      119
                                                   121

           NdeI                                                    NdeI
           |                                                       |
TTTCTTGTTCATATGATTAACTTCTAAACTTGTGTATAAATATTCTCTGAAAGTGCTTCTTTTGGCATA   207
           150                                                     206

TGTAGGTTGGGCAAAAACGAGGAAGATTGCTTCTCAATTTGGAAGAGGATGAACAGCCGAAGAAGAAAA   276

                            Sau3AI
                                DdeI
                            |   |
TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAACGGTCGTCGTCCCATGAAACAGAGGT   345
                                309
                            305
                                                            EcoRV
                                                              |
AAAACATTTTTTGCATATACACTTTGAAAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA   414
                                                            408
```

FIGURE 2A

```
                        HincII
                          HhaI
                         HaeIII
                         DdeI
                        BstEII
                         BalI                                HaeIII         AluI
                         |||                                   |              |
CAATGTCGGAGAGACAA3GGCTGMNCANCATATACAAAAGGGAAATGAAGATGGCCTTTTGATTAGCTG      483
                          439                                  469            481
                         438
                           440

           AluI                                        HinfI
           |                                            |
TGTAGCATCAGCAGCTAATCTCTGGGCTCTCATCATGGATGCTGGAACTGGATTCACTTCTCAAGTTTA      552
           498                                          535

       MspI
       HpalI                                              HinfI
       |                                                   |
TGAGTTGTCACCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAATCAATTTGATTTGT      621
       564                                                 606
       564

   DdeI
   |
AGTAAACTAAGAAGAACTTACCTTATGTTTTCCCCGCAGGACTGGATTATGGAACAATGGGAAAAGAAC      690

   629
                                             SacI
      AluI      AluI                        AluI
      |         |                          |  |
TACTATATAAGCTCCATAGCTGGTTCAGATAACGGGAGCTCTTTAGTTGTTATGTCAAAAGGTTAGTGT      759
      702       7I0                        729
                                             731
```

FIGURE 2B

```
TTAGTGAATAATAAACTTATACCACAAAGTCTTCATTGACTTATTTATATACTTGTTGTGAATTGCTAG   828

            DdeI                   HinfI
            |                      |
GAACTACTTATTCTCAGCAGTCATACAAAGTGAGTGACTCATTTCCGTTCAAGTGGATAAATAAGAAAT   897
            842                    865

          XmnI                                                 TaqI
          |                                                    |
GGAAAGAAGATTTTCATGTAACCTCCATGACAACTGCTGGTAATCGTTGGGGTGTGGTAATGTCGAGGA   966
          908                                                  961

              Sau3AI
              BclI
              |
ACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCTGGTGTTTTTATTTTCCCCTGATAGT   1035
              981

                                        AluI          RsaI
                                        |             |
CTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTGACTTTTTGTACCCAAGCGATGGGATAC   1104
                                        1074          1087

                                                     Sau3AI    AluI
                                                     |         |
ATAGGAGGTGGGAGAATGGGTATAGAATAACATCAATGGCAGCAACTGCGGATCAAGCAGCTTTCATAT   1173
                                                     1155      1165

                                                                 ScaI
                                        HinfI                    RsaI
                                        |                        |
TAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCACCGCCTTTCCAAGTA   1242
                                        1215                     1242
```

FIGURE 2C

```
                         AluI                Sau3AI                         DdeI
                          |                   |                              |
CTCATGTCAAGGTTGGTTTCTTTAGCTTTGAACACAGATTTGGATCTTTTTGTTTTGTTTCCATATACT  1311
                         1268                1285                           1311

         DdeI
    AvalI    AluI                                       HinfI      RsaI
    |    |     |                                          |          |
TAGGACCTGAGAGCTTTTGGTTGATTTTTTTTCAGGACAAATGGGCGAAGAATCTGTACATTGCATCA  1380
    1315     1325                                       1363       1370
         1319

ATATGCTATGGCAGGACAGTGTGCTGATACACACTTAAGCATCATGTGGAAAGCCAAAGACAATTGGAG  1449

     HinfI
       DdeI
     |  |
CGAGACTCAGGGTCGTCATAATACCAATCAAAGACGTAAAACCAGACGCAACCTCTTTGGTTGAATGTA  1518
       1456
     1454
                            RsaI
                              |
ATGAAAGGGATGTGTCTTGGTATGTATGTACGAATAACAAAAGAGAAGATGGAATTAGTAGTAGAAATA  1587
                            1548

         AluI                                        EcoRV
           |                                           |
TTTGGGAGCTTTTTAAGCCCTTCAAGTGTGCTTTTTATCTTATTGATATCATCCATTTGCGTTGTTTAA  1656
         1596                                        1635

       XbaI                        DdeI
        |                            |
TGCGTCTCTAGATATGTTCCTATATCTTTCTCAGTGTCTGATAAGTGAAATGTGAGAAAACCATACCAA  1725
       1664                        1687
```

FIGURE 2D

```
                                    HinfI
                                      |
ACCAAAATATTCAAATCTTATTTTTAATAATGTTGAATCACTCGGAGTTGCCACCTTCTGTGCCAATTG  1794
                                     1761

   HinfI                                                       EcoRI
     |                                                           |
TGCTGAATCTATCACACTAGAAAAAAACATTTCTTCAAGGTAATGACTTGTGGACTATGTTCTGAATTC  1863
   1800                                                         1859

TCATTAAGTTTTTATTTTCTGAAGTTTAAGTTTTTACCTTCTGTTTTGAAATATATCGTTCATAAGATG  1932

                                                SphI
    BstNI       AluI                             Sau3AI
      |           |                             |  |
TCACGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTTGTCACTCACTTCAAA  2001
     1940        1950                              1973
                                                1971

                                                   SphI
   DdeI   AluI            HhaI     NdeI    NslI                Sau3AI
     |      |               |        |      |  |                  |
CACCTAAGAGCTTCTCTCTCACAGCGCACACACATATGCATGCAATATTTACACGTGATCGCCATGCAA  2070
   2006   20I2            2028     2036   2042                2058
                                           2044

ATCTCCATTCTCACCTATAAATTAGAGCCTCGGCTTCACTCTTTACTCAAACCAAAACTCATCACTACA  2139

                              AluI
                                |
GAACATACACAAATGGCGAACAAGCTCTTCCTCGTCTCGGCAACTCTCGCCTTGTTCTTCCTTCTCACC  2208
             MetAlaAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPhePheLeuLeuThr

                                 2164
```

FIGURE 2E

```
                        TaqI                           NaeI
                           SalI                           MspI
                          HindII                          HpaII
          AccI            AccI                           HaeIII
          |              |||                            || |
AATGCCTCCGTCTACAGGACGGTTGTGGAAGTCGACGAAGATGATGCCACAAATCCAGCCGGCCCATTT  2277
AsnAlaSerValTyrArgThrValValGluValAspGluAspAspAlaThrAsnProAlaGlyProPhe
               2220                 2241                         2271
                                  2239                        2268
                                   2240                        2269

                                                      HindIII
  HinfI                                             AluI
  |                                                 | |
AGGATTCCAAAATGTAGGAAGGAGTTTCAGCAAGCACAACACCTGAAAGCTTGCCAACAATGGCTCCAC  2346
ArgIleProLysCysArgLysGluPheGlnGlnAlaGlnHisLeuLysAlaCysGlnGlnTrpLeuHis
    2281                                            2327
                                                       2325

               MspI               AvaII
                   HpaII     AvaII AluI       TaqI
               |       |       |  |     |
AAGCAGGCAATGCAGTCCGGTAGTGGTCCAAGCTGGACCCTCGATGGTGAGTTTGATTTTGAAGACGAC  2415
LysGlnAlaMetGlnSerGlySerGlyProSerTrpThrLeuAspGlyGluPheAspPheGluAspAsp
                   2364    2372   2379    2388
                                     2382

                        HaeIII                                    SacI
                          ApaI        HaeIII                    AluI
                       | |          |                          | |
GTGGAGAACCAACAACAGGGCCCGCAGCAGAGGCCACCGCTGCTCCAGCAGTGCTGCAACGAGCTCCAC  2484
ValGluAsnGlnGlnGlnGlyProGlnGlnArgProProLeuLeuGlnGlnCysCysAsnGluLeuHis
                          2438        2449                      2479
                        2436                                      2481
```

FIGURE 2F

FIGURE 2G

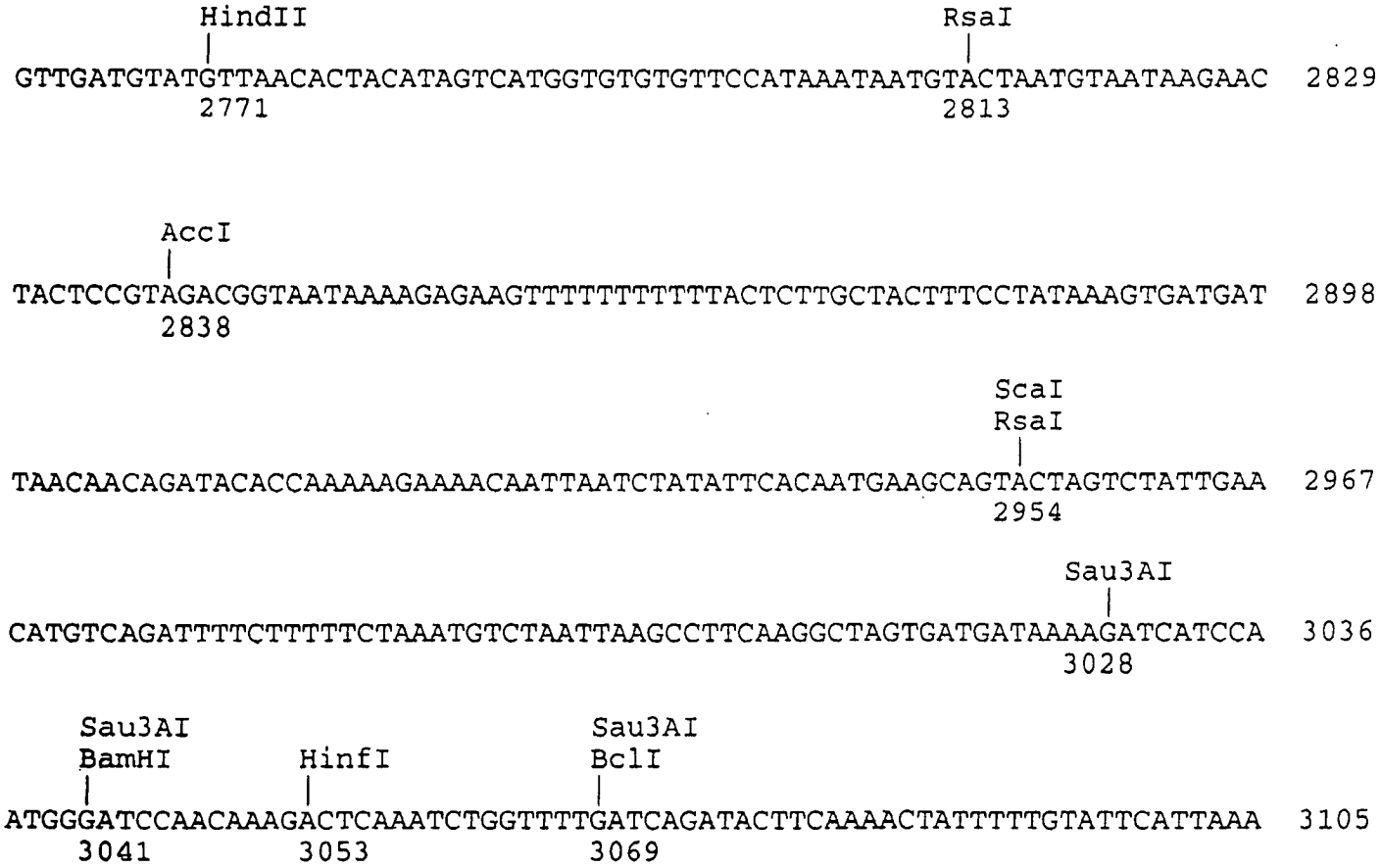

FIGURE 2H

```
                              HinfI
                                |
TTATGCAAGTGTTCTTTTATTTGGTGAAGACTCTTTAGAAGCAAAGAACGACAAGCAGTAATAAAAAAA  3174
                              3135

ACAAAGTTCAGTTTTAAGATTTGTTATTGACTTATTGTCATTTGAAAAATATAGTATGATATTAATATA  3243

GTTTTATTTATATAATGCTTGTCTATTCAAGATTTGAGAACATTAATATGATACTGTCCACATATCCAA  3312

                             NdeI
                              |
TATATTAAGTTTCATTTCTGTTCAAACATATGATAAGATGGTCAAATGATTATGAGTTTTGTTATTTAC  3381
                             3341

                         TaqI                    Sau3AI
                      AluI                  RsaI
                       |  |                   |  |
CTGAAGAAAAGATAAGTGAGCTTCGAGTTTCTGAAGGGTACGTGATCTTCATTTCTTGGCTAAAAGCGA  3450
                      3402                  3421
                         3405                  3425

ATATGACATCACCTAGAGAAAGCCGATAATAGTAAACTCTGTTCTTGGTTTTTGGTTTAATCAAACCGA  3519

                                                                MspI
 MspI  DdeI                                                     HpaII
 HpaII AluI                     NdeI               HinfI
 |      ||                        |                  |    |
ACCGGTAGCTGAGTGTCAAGTCAGCAAACATCGCAAACCATATGTCAATTCGTTAGATTCCCGGTTTAA  3588
 3522  3528                     3560               3576
        3529                                            3581
```

FIGURE 2I

```
     MspI
     HpaII
     |
GTTGTAAACCGGTATTTCATTTGGTGAAAACCCTAGAAGCCAGCCANCCTTTTTAATCTAATTTTTGCA  3657
     3598

                                    DdeI         HinfI
                                                  HincII
                                                     BstNI
                                    |            || |
AACGAGAAGTCACCACACCTCTCCACTAAAACCCTGAACCTTACTGAGAGAAGCAGAGNCANNAAAGAA  3726
                                    3702               3718
                                                  3715
                                                 3714

CAAATAAAACCCGAAGATGAGACCACCACGTGCGGCGGGACGTTCAGGGGACGGGGAGGAAGAGAATGR  3795

   AvaII
     AluI                                                        AvaII
   |  |                                                          |
CGGCGG5MNTTTGGTGGCGGCGGCGGACGTTTTGGTGGCGGCGGTGGACGTTTTGGTGGCGGCGGTGGA  3864
      3804                                                       3863
   3801

         EcoRV        AvaII                                    DdeI
         |            |                                        |
CCTTTGGTGGTGGATATCGTGACGAAGGACCTCCCAGTGAAGTCATTGGTTCGTTTACTCTTTTCTTAG  3933

         3880         3892                                     3930
```

FIGURE 2J

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FIGURE 2K

4325

TaqI
SalI
PstI
HincII
HindIII
Sau3AI AluI
AccI EcoRI

TGGGAAAGTTGATGAGATCCAAGCTTGGGCTGCAGGTCGACGAATTC

4294 4302 4316 4321
4300 4314
4313
4315

FIGURE 2L

Brassica campestris ACP Genomic Sequence

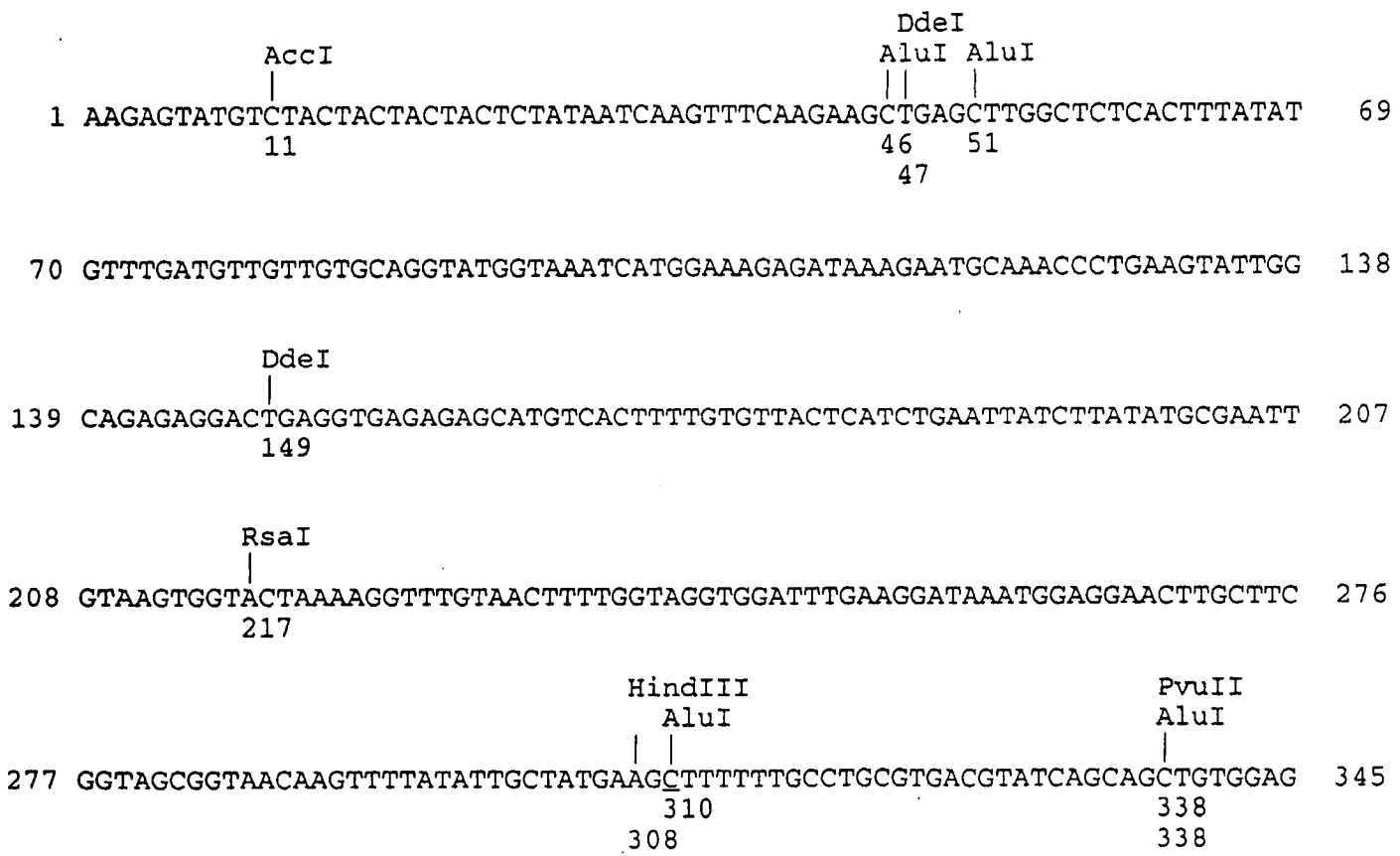


FIGURE 3A

```
                                MspI
                                HpaII
                                HaeIII
                                ||
346 AAGATGGTATTAGAAAGGGTCTTTTCACATTTTGTGTTGTGACAAATATTAATTCGGCCGGTATGGTTT  414
                                  403
                                  404
                                  404

415 GGTTAAGACTTGTTGAGAGACGTGTGGGGTTTTTTGATGTATAATTAGTCTGTGTTTAGAACGAAACAA  483

                                                    Tth111I
                                                    |
484 GACTTGTTGNGTATGCTTTTTTTTAACTTGAGGGGGTTTGTTGTTAGTTAGGAACTTGACTTTGTCT  552
                                                      547

                                    ScaI
                                    RsaI
                                    |
553 CTTTCTCTCAAGATCTGATTGGTAAGGTCTGGGTGGTAGTACTGTTTGGTTTAATTTGTTTTTGACTATT  621
                  564
                  564
                  593
                  593

                                                    HpaII
                                                    DraI MspI DdeI
                                                    |    |    |
                  HinfI     HaeIII     DraI
                  |         |          |
622 GAGTCACTGTGGCCCATTGACTTTAAATTAGGCTGGTATATTTTTTGGTTTAAAACCGGTCTGAGATAG  690
                  623       634        646          673  678  683
                                                      678
```

FIGURE 3B

```
                TaqI
                  HinfI                      DraI
                |  |                          |
691 TGCAATTTCGATTCAGTCAATTTTAAATTCTTCAAGGTAATGGGCTGAATACTTGTATAGTTTTAAGAC  759
                   701                        715
                699

                StuI
                HaeIII          HaeIII                                            HindIII
                |               |                                                   AluI
                                                                                  |  |
760 TTAACAGGCCTTAAAAGGCCCATGTTATCATAAAACGTCATTGTTTAGAGTGCACCAAGCTTATAAAAT  828
                768             778                                                  819
                768                                                               817

                 StuI
                 HaeIII                      StuI
             BstNI                           HaeIII                            HaeIII
             |   |                           |                                 |
829 GTAGCCAGGCCTTAAAAGACTTAACAGGCCTTAAAAGACTTAACATTCCTTAAAAGGCCCATGTTATCA  897
             835                             857                               886
                 838                         857
                 838

                                                           StuI
                                                           HaeIII                      StuI
                                             AluI     BstNI                            HaeIII
                                             |        |   |                            |
898 TAAAACGTCATCGTTTTGAGTGCACCAAGCTAAATGTAGCCAGGCCTTAAAAGACTTAACAGGCCTTAA  966
                                             927      939                              961
                                                          942                          961
                                                          942
```

FIGURE 3C

```
                                                   HindIII
     HaeIII                                          AluI                AluI AvaI
      |                                             | |                    |    |
967 AAGGCCCATGTTATCATAAAACGCCGTCGTTTTGAGTGCACCAAGCTTATAAATGTAGCCAGCTACCTC 1035
      971                                            1012                1029 1034
                                                    1010

                                                   XhoI
                                                    TaqI  Sau3AI
                     RsaI                          AvaI   BglII   AvaI      TaqI
                      |                            ||      |       |         |
1036 GGGACATCACGCTCTTTGTACACTCCGCCATCTCTCTCTCTCTCGAGCAGATCTCTCTCGGGAATATCG 1104
                      1055                         1078    1085   1093      1103
                                                    1079   1085
                                                   1078

       Tth111I
           TaqI
          SalI
         HincII
           AccI
       |  |||
1105 ACAATGTCGACCACTTTCTGCTCTTCCGTCTCCATGCAAGCCACTTCTCTGGTAATCTCATCTCCTTCT 1173
       METSerThrThrPheCysSerSerValSerMETGlnAlaThrSerLeu
           1112
         1110
          1111
           1112
       1108
```

FIGURE 3D

```
                 Sau3AI
         Sau3AI  BclI                 Sau3AI          Sau3AI
         |       |                    |               |
1174 TGTGTTCCCAGATCGCTCTGATCATACTTTCTTTTAGATCATTTGCCTCTGATCTGTTGCTTGATGTTT 1242
         1184    1193                 1210            1224
                 1193

     HincII                                                  AluI    HinfI
     |                                                       |       |
1243 GTTAACTCTCCACGCATGTTTGATTATGTTGAGAATTAGAAAAAAAATGTTAGCTTTACGAATCTTTAG 1311
     1243                                                    1296    1303

      Sau3AI                                                       TaqI
      BclI                                                          Sau3AI
      |                                                            ||
1312 TGATCATTTCAATTGGATTTGCAATCTTGTGTGACATTTGAGGCTTGTGTAGATTTCGATCTGTATTCA 1380
      1313                                                          1369
      1313                                                         1368

         HinfI   AluI                                  DraI
         |       |                                     |
1381 TTTTGAATCACAGCTATAATAGTCATTTGAGTAGTAGTGTTTTTAAATGAACATGTTTTGTTGTATTGA 1449
         1386    1394                                  1425

                                                         AluI
                                                         |
1450 TGGAACAAACAGGCAGCAACAACGAGGATTAGTTTCCAGAAGCCAGCTTTGGTTTCAACGACTAATCTC 1518
                 AlaAlaThrThrArgIleSerPheGlnLysProAlaLeuValSerThrThrAsnLeu
                                                         1496
```

FIGURE 3E

```
                                                             HhaI                DdeI
                                                             |                   |
1519 TCCTTCAACCTCCGCCGTTCAATCCCCACTCGTTTCTCAATCTCCTGCGCGGTATGTTCTCATTCTCAG 1587
     SerPheAsnLeuArgArgSerIleProThrArgPheSerIleSerCysAla
                                                             1568                1584

           TaqI
           |    AluI                RsaI                                   HaeIII
           |    |                   |                                      |
1588 CATTTATTTCGAGCTTGCTTGTCATGGTACTCTCTCTAATTGTCTATTTGGTTTATTAGGCCAAACCAG 1656
                                                                     AlaLysProG
                1601                1616                                   1648
           1597

                       DdeI                     AluI
                       |                        |
1657 AGACGGTTGAGAAAGTGTCTAAGATAGTTAAGAAGCAGCTATCACTCAAAGACGACCAAAAGGTCGTTG 1725
     luThrValGluLysValSerLysIleValLysLysGlnLeuSerLeuLysAspAspGlnLysValValA
                       1676                     1695

                    Sau3AI           HinfI   TaqI
                    |                |       |
1726 CGGAGACCAAGTTTGCTGATCTTGGAGCAGATTCTCTCGACACTGTAAGTCATCAATCATTCTCTTATG 1794
     laGluThrLysPheAlaAspLeuGlyAlaAspSerLeuAspThr
                    1743             1756    1763

                                                DdeI                SphI
                                                |                   |
1795 TGAATAAAGAGAACTTGAAGAGTTTGTTTTTAACATATTAACTGAGTGTTTTGCATGCAGGTTGAGATA 1863
                                                                      ValGluIle
                                                 1837                1852
```

FIGURE 3F

```
                                                    TaqI                                     DdeI
                                                  EcoRV                                    AluI
                                                    | |                                      ||
1864 GTGATGGGTTTAGAGGAAGAGTTTGATATCGAAATGGCTGAAGAGAAAGCTCAGAAGATTGCTACTGTG 1932
     ValMetGlyLeuGluGluGluPheAspIleGluMetAlaGluGluLysAlaGlnLysIleAlaThrVal
                                  1891                         1913
                                    1893                        1914

                                                    SacI
              AluI                                AluI
                |                                   | |
1933 GAGGAAGCTGCTGAACTCATTGAAGAGCTCGTTCAACTTAAGAAGTAATTTTAGTATTAAGAGCAGCCA 2001
     GluGluAlaAlaGluLeuIleGluGluLeuValGlnLeuLysLys
              1940                1960
                                    1962

                                                                                   HinfI
                                                                                     |
2002 AGGCTTTGTTGGGTTTGTTGTTTTCATAATCTTCCTGTCATTTTCTTTTTCTTTAATGTGTCAAGCGAC 2070
                                                                             2069

                                                                       TaqI
                                                                      SalI
                                                    Sau3AI           HincII
              DraI                             NcoI                    AccI
                |                               |   |                 |||
2071 TCTGTTGGTTTAAAGTAGTATCTGTTTGCCATGGATCTCTCTCTATTTGTCGACTGAAAACTTTTGGTT 2139
                2082                          2100                    2121
                                                    2104             2119
                                                                      2120
                                                                      2121

            HindIII
              AluI
             |  |
2140 TACACATGAAAGCTT 2154
                 2152
             2150
```

FIGURE 3G

Brassica Campestris Seed Specific cDNA-EA9

```
                                          Sau3AI
                                            |
  1 TTCAACTTTTCTAAACCAAATGGCTTTAACACAGATCCAAATCTTTCTCATTGTCTCTCTAGTCTCATC   69
                          METAlaLeuThrGlnIleGlnIlePheLeuIleValSerLeuValSerSe
                                          34

                  TaqI
                   Sau3AI
                  ClaI                          TaqI
                  ||                             |
 70 ATTCAGTTTATCGATCACTCTTTCTCGTCCATTACTCGATGAAGTCGCCATGCAAAAGAGACATGCCGA  138
    rPheSerLeuSerIleThrLeuSerArgProLeuLeuAspGluValAlaMETGlnLysArgHisAlaGl
                  81                            106
                   82
                  81

                         HaeIII
                           |
139 GTGGATGACCGAACACGGCCGTGTTTACGCAGATGCGAACGAGAAAAACAACCGCTACGCTGTTTTCAA  207
    uTrpMETThrGluHisGlyArgValTyrAlaAspAlaAsnGluLysAsnAsnArgTyrAlaValPheLy
                         157
```

Complete nucleotide sequence of B. campestris cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of the sequence and a potential polyadenylation signal is underlined.

FIGURE 4A

```
                                                      HpaII          DraI
                                                      |              |
208 ACGCAACGTGGAACGCATTGAACGCTTAAATGACGTTCAATCCGGACTAACGTTTAAACTCGCGGTGAA  276
    sArgAsnValGluArgIleGluArgLeuAsnAspValGlnSerGlyLeuThrPheLysLeuAlaValAs
                                                      250            263

           Sau3AI            EcoRI            RsaI
           |                 |                |
277 CCAGTTTGCTGATCTAACCAACGAAGAATTCCGTTCTATGTACACTGGTTTCAAAGGAAACTCTGTGTT  345
    nGlnPheAlaAspLeuThrAsnGluGluPheArgSerMETTyrThrGlyPheLysGlyAsnSerValLe
           287               303              318

                                      RsaI
        TaqI                           KpnI                        HpaII
        |                             |  |                         |
346 GTCTAGTCGAACTAAACCAACGTCGTTTAGGTACCAAAACGTTTCTTCTGATGCGTTGCCGGTTTCTGT  414
    uSerSerArgThrLysProThrSerPheArgTyrGlnAsnValSerSerAspAlaLeuProValSerVa
        353                            380                         405
                                      378

                      AluI                  Sau3AI            Sau3AI
                      |                     |                 |
415 TGATTGGAGGAAGAAAGGAGCTGTGACTCCTATCAAGGATCAAGGCTTATGCGGATCTTGTTGGGCGTT  483
    lAspTrpArgLysLysGlyAlaValThrProIleLysAspGlnGlyLeuCysGlySerCysTrpAlaPh
                      435                   452               468
```

FIGURE 4B

```
          PvuII
          AluI
           |
484 TTCAGCTGTTGCGGCTATAGAAGGAGTAGCACAGATAAAGAAAGGGAAACTCATTTCTTTGTCTGAACA  552
    eSerAlaValAlaAlaIleGluGlyValAlaGlnIleLysLysGlyLysLeuIleSerLeuSerGluGl
          489
          489

                TaqI
             SalI
                HincII
             AluI AccI
              |  |||
553 AGAGCTTGTCGACTGCGACACAAACGATGGTGGCTGCATGGGCGGTTTGATGGATACAGCGTTTAACTA  621
    nGluLeuValAspCysAspThrAsnAspGlyGlyCysMETGlyGlyLeuMETAspThrAlaPheAsnTy
          557   562
                560
                561
                562

622 CACAATAACTATTGGCGGCTTAACCTCTGAATCAAATTATCCTTATAAAAGCACAAACGGCACTTGCAA  690
    rThrIleThrIleGlyGlyLeuThrSerGluSerAsnTyrProTyrLysSerThrAsnGlyThrCysAs

                      HpaII
                       |
691 CTTCAATAAAACTAAACAGATAGCAACTTCTATCAAAGGTTTTGAGGATGTCCCGGCTAACGATGAGAA  759
    nPheAsnLysThrLysGlnIleAlaThrSerIleLysGlyPheGluAspValProAlaAsnAspGluLy
                      744
```

FIGURE 4C

```
                                     HpaII
                                     |
760 AGCCCTAATGAAGGCAGTGGCACACCACCCGGTTAGCATTGGAATAGCGGAGGAGATATTGGTTTCCA  828
    sAlaLeuMETLysAlaValAlaHisHisProValSerIleGlyIleAlaGlyGlyAspIleGlyPheGl
                                     789

                                                     Sau3AI
                 HpaII                               BclI
                 |                                   |
829 ATTCTATTCGTCCGGTGTGTTCAGCGGAGAATGCACAACTCATCTTGATCACGGGGTAACTGCGGTTGG  897
    nPheTyrSerSerGlyValPheSerGlyGluCysThrThrHisLeuAspHisGlyValThrAlaValGl
                 841                                 875
                                                     875

                                     ScaI
                                         Sau3AI
         Sau3AI                      RsaI
       HaeIII                            BamHI     EcoRI     AvaII
       |  |                          |   |         |         |
898 ATACGGCCGATCTAAAAACGGATTAAAGTACTGGATCCTCAAGAATTCATGGGGACCAAAATGGGGAGA  966
    yTyrGlyArgSerLysAsnGlyLeuLysTyrTrpIleLeuLysAsnSerTrpGlyProLysTrpGlyGl
       904                               931       941       951
          906                        927
                                         931
                                     927

                 Sau3AI        EcoRV
                 |             |
967 ACGTGGATACATGAGGATCAAAAAAGATATCAAGCCTAAACACGGACAATGTGGTCTTGCCATGAATGC 1035
    uArgGlyTyrMETArgIleLysLysAspIleLysProLysHisGlyGlnCysGlyLeuAlaMETAsnAl
                 982           995
```

FIGURE 4D

```
                HindIII
   RsaI          HpaII  AluI
     |              |     | |
1036 TTCGTACCCAACTATGTGAAAAAATCGGTTCAATATCCGGTTAAGCTTTAGAATAAATGTGTGTGTTGG 1104
     aSerTyrProThrMET
       1041                1073    1081
                                 1079

1105 TTATAATTTAAGACTCTGTTGCATGTAATTTGTGAAATGGTAAGTTTATGTGATGCAAAAGATTTGATA 1173

1174 AAAAAAAAAAAAA 1186
```

FIGURE 4E

```
3H11  TTTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA  51

3H11  GCTTACAGCTGGGAGAACATTGTCTAACTCTTCTGAAATTTAAATGTTATC 102

3H11  CAGAATCCTTCATCATAAAATAATATCAAAATGCAAATCTATTTTTTCTAC 153

3H11  TCTTGTCTAGCTTCAACTTTCTTCTTCTGCTCATCAATTAGCAATTAATCC 204
                                    TGCTCATCAATTAGCAATTAATCC

3H11  AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC 255
2A11  AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC
            METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe

3H11  GTTGTTCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTCGAAAATG 306
2A11  GTTGTTCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTCGAAAATG
      ValValLeuLeuThrThrThrLeuValAspMETSerGlyIleSerLysMET

3H11  CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG 357
2A11  CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG
      GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET

3H11  AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA 408
2A11  AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA
      LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer

3H11  AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG 459
2A11  AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG
      AsnSerAspCysIleGlyIleThrLeuCysGlnPhyCysLysGluLysThr

3H11  GACCAGTATGGTTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA 510
2A11  GACCAGTATGGTTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA
      AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro

3H11  TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA 561
2A11  TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA

3H11  TAGTGTTGTCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612
2A11  TAGTGTTGTCTGTACCTTTGGTGTGAAGAATGTGAATAAAGGGATACATAT

3H11  ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT 663
2A11  ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT

3H11  GATTGTTTGAATAAAAACATACCATGAGTGAAATAATTATTCCACATTAAT 714
2A11  GATTGTTTGAATAAAAACATACCATGAGTGAAATAATTATTCC

3H11  TCACGTATTTATTTCACTTATGATACGTATTTTTGTTCCTTTCGCGTAAAA 765
3H11  AAAAAAAAA  774
```

FIGURE 5

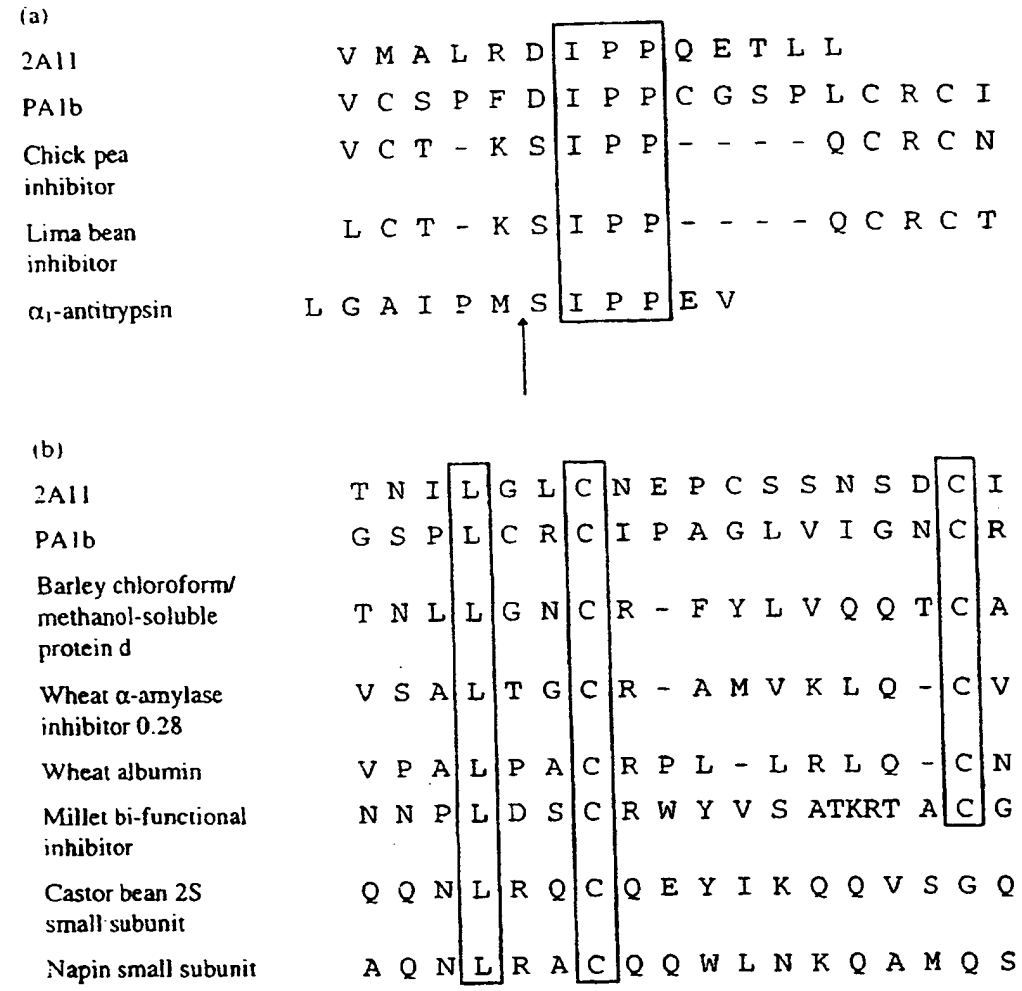


FIGURE 6

2A11 GENOMIC

```
CTCGAGCCCT TTAAAAAGTA TAGTCAATAT TTACGGTGAC CGTGAATTTC TTAATTATGA   60
TATATAATTT AAAAGAAATC ATGATCACAT TCTACTGATG AGAACATGTG CTAATCAAGG  120
GAAAACATGG ATGTGAAAAA TACTTTTTGT TAAAAGTAAA AAAAAATGTG AAATTTTGTT  180
AGTTATTTAC TACCTATACA TTATTTGAGC ATGTGCAAAC TTTACAAATA CCTAATAGAA  240
GATTTTCACC TGCCTGTATA TATGTAAATT AATTATAATG AACACTCTCA CATAAAATAA  300
TTATCAGTAT ATACATTAAT ACTTGCCCTC CACAATGAAT TAAATAAAAT GTAGAACATG  360
ATCTACACTT CAATAAAACT AAGACCATAA AGAATAATTT CAAAATATAC ACATGTCAAC  420
AATAAATTAT TTGCATATTA TATTAACTTA CTAAACAATC TTTACTTTTG AAATATAAAA  480
ATAATCAAGT TATAAGTCTG CTCAAAGTAA AGCACTTGTT AGACTCATCT GATTTTGAGA  540
AGGTAAGCAA ATTGATGGTG CATAATAGTC ACAAGTAAAA TATAAAATAG ATTTCATTAG  600
TAAAATTGTT TTTTACTTTC TTTATATATA ATTATCAATA TCCTTCAATG GTAGGTTAAT  660
TATATTGTTA ACTTCTTGTT GAATTAAAGC AATAAGACAA GAATATTAAA GATAAAAGAA  720
CAATAAAAAT AGAAAGACTA AGAGATAAGA GTTTTCTTAT TCTTCTTTCA ATAAGTATCA  780
TCAAGTGTAT ACAATATAAA TTTTTGTATT TTTGATCTAT CTATTTATAA TGTTATATAT  840
AAGCATACAA AAGATCAGTC ATAAATATGA CTTTAATCAT GAAAATAATG AAAGAGATTA  900
```

FIGURE 7A

```
TGAAGGCGTA AGGTTACTAG AATAATAGTC ATTAAAAAAA GGGGTTATCT TTATAATTGA   960

ATAATTGATG AAGTAATGGA GATAATTAGT GAGCATAAAT TTTTTTAAAA AAATGGACAT  1020

TTACACTATA ATATTTTATA ACACTTTCCC TTAAACATCT AGGTATAAAT AATGAGTCTT  1080

GTCAAAATCT TAGTAGGAAA AATTCTGTGA AATTTTTTTA GTGAAAACAA ATGATATAAA  1140

TATCTTGAAT ACTCATTATT TGTTGTCTCA TTAAAAATCT TATCTGACCT ATAAAATAAA  1200

TTATTTGCTC AACTCAAAAT AGTTTTTCAT TCTAAAATTA GTATAATTAT TAGTGAATAT  1260

TTAATTAACA TAATTGTATA CTAAGGGGCC TATAAATTGG ATTCTTCTCA AAGAAAAATA  1320

AAATCACCAC ACAACTTTCT TCTTCTGCTC ATCAATTAGC AATTAATCCA AAACCATT    1378

ATG GCT GCC AAA AAT TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT GTT     1426
MET Ala Ala Lys Asn Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val

CTT TTG ACG ACC ACT TTA GGTTCACAAC ACTTCTCCCT TATTTTGTTT           1474
Leu Leu Thr Thr Thr Leu

TCTTAATTTC TTGGAAGTCA TATGCATGTG TTTGGTATCA TGGTATATAT ATAAAGGAAA  1534

ATATTTTTCT TAATTACTGG TTTTCTAATG TTTGGTAGGT AATCGGAAAT TATTATGAGA  1594

TAATGAACTT GCAAAGTCAT TATTATATAA CTTTTTTTTT ATACTTTGAT TTAAGAATTC  1654

ATTTTTCTCA TTTTATATAA ACTTATTTTT CAACAGAAAA TATTTTTCGA ACTATTCAAA  1714

CACACCCTAA GACATTACAT ATATATATAT ATACACCCTC CGTTTTATAT TACTTAATGC  1774
```

FIGURE 7B

```
CTATTGAGTT GGCCCACCCT TTAAGAATGA TTCAATTAGA GATATGTTTT ACTAAATTAA  1834

CCTATGCTTT AAGACTCTAA ATTTGGCTAT TACTATTTTA CGTTGTAATT TAATGACAAA  1894

CATTTCATAA TGACTATAGT CTGAACTTAA TTAGACAGAC GTATCTATAG TTTGCTTACT  1954

AATGATTCAT AGCTATATAT TTGGAGAGGA GAGAGACAAA CGATATTAAG AAAGGGAGGA  2014

GAGAGGCGAG GTAAATCTGA AATAGAGAAG AGAAAGGCAA CCAATTTTGA TCATCTATCA  2074

TACTTTTGAT TATTATTTTT ATTATATGTA CGTTTACATT ACAGTTTTCG AATTCTTACA  2134

TTAATCTTAA TCATAATATA TACA GTT GAT ATG TCT GGA ATT TCG AAA ATG CAA  2188
                          Val Asp MET Ser Gly Ile Ser Lys MET Gln

GTG ATG GCT CTT CGA GAC ATA CCC CCA CAA GAA ACA TTG CTG AAA ATG    2236
Val MET Ala Leu Arg Asp Ile Pro Pro Gln Glu Thr Leu Leu Lys MET

AAG CTA CTT CCC ACA AAT ATT TTG GGA CTT TGT AAC GAA CCT TGC AGC    2284
Lys Leu Leu Pro Thr Asn Ile Leu Gly Leu Cys Asn Glu Pro Cys Ser

TCA AAC TCT GAT TGC ATC GGA ATT ACC CTT TGC CAA TTT TGT AAG GAG    2332
Ser Asn Ser Asp Cys Ile Gly Ile Thr Leu Cys Gln Phe Cys Lys Glu

AAG ACG GAC CAG TAT GGT TTA ACA TAC CGT ACA TGC AAC CTG TTG CCT    2390
Lys Thr Asp Gln Tyr Gly Leu Thr Tyr Arg Thr Cys Asn Leu Leu Pro

TGA ACAATATCAA TGATCTATCG ATCGATCTAT CTATCTATTT ATCTGTCTCT          2433

GCGCGTATAG TGTTGTCTGT ACCTTTGGTG TGAAGAATAT GAATAAAGGG ATACATATAT  2493

CTAGATATAT TCTAGGTAAT GTCCTATTGT ATTTAAAATT TGTAGCAATG ATTGTTTGAA  2553
```

FIGURE 7C

TAAAAACATA	CCATGAGTGA	AATAATTATT	CCACATTAAT	TCACGTATTT	ATTTCACTTA	2613
TGATACGTAT	TTTGTTCCT	TTCGCGTAGA	TTTTTGATCC	TTTTCCCTTT	TGAATATTAA	2673
ACATTAAACA	CAAATAATGT	TTATTAAATT	AAGTTAATAT	TTTTATTTAG	CTATTTATAT	2733
TTTTATTTGA	AATCAAACTT	GATAAATATT	TATAAAGATA	ATTAACAAGT	AATGTGACAC	2793
TAACACCATG	TAATATTATC	TTGTCGTTAT	TTATGATAAT	ATTTTAAAAT	TATAATTTCA	2853
GTTAAAAAAT	TATTAAAAAA	ACATACTTTT	AAAAAGTGAG	TTAGCCTCCG	CTACCCACAT	2913
ACTTATGAAT	TGGACTAGTT	GTTTTTTGAC	CCACAAAAAG	AATGGGCTAA	TTAAACCTGA	2973
CCTATCAAAT	TTCAGAATCT	GCATAGATTA	GTCCGAACGA	AATGAGTCAG	CCCGTATTGA	3033
ACAAAATATC	AACAAGGACG	TTATGTAAAG	ATGTTTAAGA	AGGAAAAAAG	ATTTCTAATA	3093
CATATGGACT	TTCAATATCC	CAACTTTGTC	TGGCGATCTG	AACCCTGCTT	AGTTTGTTGA	3153
TCATTAACTT	GTCTTGCTAT	GTATTTAAGA	TTTAAACTTT	ATATGTTTAA	ACTTACAGAA	3213
AATACATATA	AATCTCTCAA	GACTTGGCAA	CATAATTTAC	TTTAGTACTT	AAACTACATG	3273
AAAATTTAAA	TATCCTTTTA	ACATCTTTGA	AGTGAATTAA	ATTATCACAA	TCCGAGCCTA	3333
CACCTTGGAC	GTGGCCGGCA	CTCAAGAACC	AGTGCTGGTC	CCCAAGCTAA	CCCTCATCCT	3393
GACTGACTAC	AAGCGGAAGG	CTAACTTAAG	TATACAAAAG	CTTAAAACTG	AATAAAATAA	3453
ACTTTACAAG	GTTTTAACAC	AAATGAACAA	CTTTGAAGAA	AATAATATAT	TCAACTAGCC	3513

FIGURE 7D

ATAAAATAGA CAACTTTAGT CTTTAAAACA TTTAATAAAA TAAATGCAAA ATATAGACTC 3573
CTTAACTAAA CTGACTATCT ATGGAGCCTC TAATTGATAA AGATGGAAGT CGGGACAAGA 3633
CCACGACATC CTGACTAAAC TGAGAAGTAA ATAAAATCCC CCGGAAAAAA AGGAGCCTCA 3693
CCATGGCTAA CTCGAACTCG GGGATATATC AATGAAGCTC CTGTTGATGA TCTTGAAGAC 3753
ATGTCTCTGC ATCATCAAAA AGATGCAGGC CAAATGGCTC AGTACGTAAA ATGTACGAGT 3813
ATGTAAGGGA AATTCTAAAG TATAACATAA GCTTGATACT TGAATAAAAG GAAACATACT 3873
TACCTCTTTT CAACTCAACT CAAATTAAGA ATAAGATACT CAACTCAAAG ATTAGGTATT 3933
CAACGCAAAT ATGGCACTCT ACTCAATGAA GTACAAATTA ACTCAGGATA CTCGACTTAA 3993
GATACTCAAC TCCCGACACT CAACTGAACT CATTTCAATA TAAAGCAGCT TAAAACAAGT 4053
TCAGTATAAA GTAAAGTTGT TTAAAAACAT GATGTCAACT CTGTGTGTAT AATAAGGGAT 4113
ACAACATAAC TTTGAAATGT ATATAAAAAT ACAATTAACT GATGTATATA AAAATACATT 4173
AATCTATGGG AGATTCTCTA ACCGACAACC ATCACTTAAG GGCTAAGATG ATGATATAGC 4233
GATCTACCGC ACGCTGCCAT CGCATCTTAT ACCCGGCCAA AGGTATAAGA CCTGAACTGC 4293
CTAATGAATC CACTAATAAA CTGTTAAAAG GAATCATCTA AAAAGTATGA CCCTTTTCTA 4353
CCCATAGTGG CTAACATGGT TTATGGGGGC TGTGAGTTAT CTGAACTCTC CCCCATATCG 4413

FIGURE 7E

GTGCTCAATA CTACTCCAAA AAATATACTG CTCTTATGTT TAAAAACATA CTGATTCTGT 4473

GGTTTGAAAT TATTGCTTAA AGCTTAGATT TTTGAAAAGC TCTCTTTTGA AAATCGTAGT 4533

TTCCTTTTTC TTCTATTAAA GCTAGACATA GGCTATGTAG AACTCTAGCT TACCTTCCTT 4593

CTCAAAAGTT TGAAAACATT TGCTTAGATT CTTAGGGACT ACTTAGTTCC CTTGTTGGAA 4653

TTC 4656

FIGURE 7F

PG GENOMIC

```
        10          20          30          40          50          60
                                                                      *
AAGCTTCTTA AAAAGGCAAA TTGATTAATT TGAAGTCAAA ATAATTAATT ATAACAGTGG

        70          80          90         100         110         120
                                                                      *
TAAAGCACCT TAAGAAACCA TAGTTTGAAA GGTTACCAAT GCGCTATATA TTAATCAACT

       130         140         150         160         170         180
                                                                      *
TGATAATATA AAAAAAATTT CAATTCGAAA AGGGCCTAAA ATATTCTCAA AGTATTCGAA

       190         200         210         220         230         240
                                                                      *
ATGGTACAAA ACTACCATCC GTCCACCTAT TGACTCCAAA ATAAAATTAT TATCCACCTT

       250         260         270         280         290         300
                                                                      *
TGAGTTTAAA ATTGACTACT TATATAACAA TTCTAAATTT AAACTATTTT AATACTTTTA

       310         320         330         340         350         360
                                                                      *
AAAATACATG GCGTTCAAAT ATTTAATATA ATTTAATTTA TGAATATCAT TTATAAACCA

       370         380         390         400         410         420
                                                                      *
ACCAACTACC AACTCATTAA TCATTAAATC CCACCCAAAT TCTACTATCA AAATTGTCCT

       430         440         450         460         470         480
                                                                      *
AAACACTACT AAAACAAGAC GAAATTGTTC GAGTCCGAAT CGAAGCACCA ATCTAATTTA

       490         500         510         520         530         540
                                                                      *
GGTTGAGCCG CATATTTAGG AGGACACTTT CAATAGTATT TTTTTCAAGC ATGAATTTGA
       550         560         570         580         590         600
                                                                      *
AATTTAAGAT TAATGGTAAA GAAGTAGTAC ATCCCGAATT AATTCATGCC TTTTTTAAAT

       610         620         630         640         650         660
                                                                      *
ATAATTATAT AAATATTTAT GATTTGTTTT AAATATTAAA ACTTGAATAT ATTATTTTTT

       670         680         690         700         710         720
                                                                      *
TAAAAATTAT CTATTAAGTA CCATCACATA ATTGAGACGA AGGAATAATT AAGATGAACA
       730         740         750         760         770         780
                                                                      *
TAGTGTTTAA TTAGTAATGG ATGGGTAGTA AATTTATTTA TAAATTATAT CAATAAGTTA

       790         800         810         820         830         840
                                                                      *
AATTATAACA AATATTTGAG CGCCATGTAT TTTAAAAAAT ATTAAATAGT TTGAATTTAA
```

FIGURE 8A

```
      850         860         870         880         890         900
                                                                    *
AACCGTTAGA TAAATGGTCA ATTTTGAACC CAAAAGTGGA TGAGAAGGGT ATTTTAGAGC

      910         920         930         940         950         960
                                                                    *
CAATAGGRGG ATGAGAAGGA TATTTTGAAG CCAATATGTG ATGGATGAAG GATAATTTTG

      970         980         990        1000        1010        1020
                                                                    *
TATCATTTCT AATACTTTAA AGATATTTTA GGTCATTTTC CCTTCTTTAG TTTATAGACT

     1030        1040        1050        1060        1070        1080
                                                                    *
ATAGTGTTAG TTCATCGAAT ATCATCTATT ATTTCCGTCT TAAATTATTT TTTATTTTAT

     1090        1100        1110        1120        1130        1140
                                                                    *
AAATTTTTTA AAAATAAATT ATTTTTTCCA TTTAACTTTG ATTGTAATTA ATTTTTAAAA

     1150        1160        1170        1180        1190        1200
                                                                    *
ATTACCAACA TATAAATAAA ATTAATATTT AACAAAGAAT TGTAACATAA TATTTTTTTA

     1210        1220        1230        1240        1250        1260
                                                                    *
ATTATTCAAA ATAAATATTT TTAAACATCA TATAAAAGAA ATACGACAAA AAAATTGAGA

     1270        1280        1290        1300        1310        1320
                                                                    *
CGGGAGAAGA CAAGCCAGAC AAAAATGTCC AAGAAACTCT TTCGTCTAAA TATCTCTCAT

     1330        1340        1350        1360        1370        1380
                                                                    *
CCAAACTAAT ATAATACCCA TTATAATTAA CCATATTGAC CAACTCAAAC CCCTTAAAAT

     1390        1400        1410        1420        1430        1440
                                                                    *
CTATAAATAG ACAAACCCTT CCCATACCTC TTATCATAAA AAAAATAATA ATCTTTTTCA

     1450        1460        1470        1480        1490        1500
                                                                    *
ATAGACAAGT TTAAAAACCA TACCATATAA CAATATATCA TGGTTATCCA AAGGAATAGT

     1510        1520        1530        1540        1550        1560
                                                                    *
ATTCTCCTTC TCATTATTAT TTTTGCTTCA TCAATTTCAA CTTGTAGAAG CAATGTTATT

     1570        1580        1590        1600        1610        1620
                                                                    *
GATGACAATT TATTCAAACA AGTTTATGAT AATATTCTTG AACAAGAATT TGCTCATGAT

     1630        1640        1650        1660        1670        1680
                                                                    *
TTTCAAGCTT ATCTTTCTTA TTTGAGCAAA AATATTGAAA GCAACAATAA TATTGACAAG
```

FIGURE 8B


```
      1690        1700        1710        1720        1730        1740
                                                                     *
GTTGATAAAA ATGGGATTAA AGTGATTAAT GTACTTAGCT TTGGAGCTAA GGGTGATGGA

      1750        1760        1770        1780        1790        1800
                                                                     *
AAAACATATG ATAATATTGT AAGTATTTAA ATATTGGAAT ATATTTGTGG GGATGAAAAT

      1810        1820        1830        1840        1850        1860
                                                                     *
GATAGAGAAT ATAAGAATTA TTTGGAAGGA TGAAAAGTTA TATTTTATAA AGTAGAAAAT

      1870        1880        1890        1900        1910        1920
                                                                     *
TATTTTCTCG TTTTTAGTAA TTAAAGGTGA AAAATGAGTT TTCTCGTAAG CGAGGAAAGT

      1930        1940        1950        1960        1970        1980
                                                                     *
CATTTTCCAT GGAACTGTAT TTTTTTTTTA CTTTTAATAA CGTCATAGTA TTTGCTATAC

      1990        2000        2010        2020        2030        2040
                                                                     *
TCAAGAATAA GACACTATTA TTGATGTTTA GTGCTCGAAA AGAAATTGAT AGTAATTTTG

      2050        2060        2070        2080        2090        2100
                                                                     *
CTAATATAAC TATCAATTTC TTATATGTAT ATTTTTCAAC CAAAATAACA AAGCGTAATC

      2110        2120        2130        2140        2150        2160
                                                                     *
CAATAAGTGG GCCTCTAGAA TAAAGAGTAA GTTCTATTAA TTCTTAACCT TATTTAATTT

      2170        2180        2190        2200
TATGGAAACC TCGACAAAAC GACAATGCTC AACTTATATT CGAATTC
```

FIGURE 8C

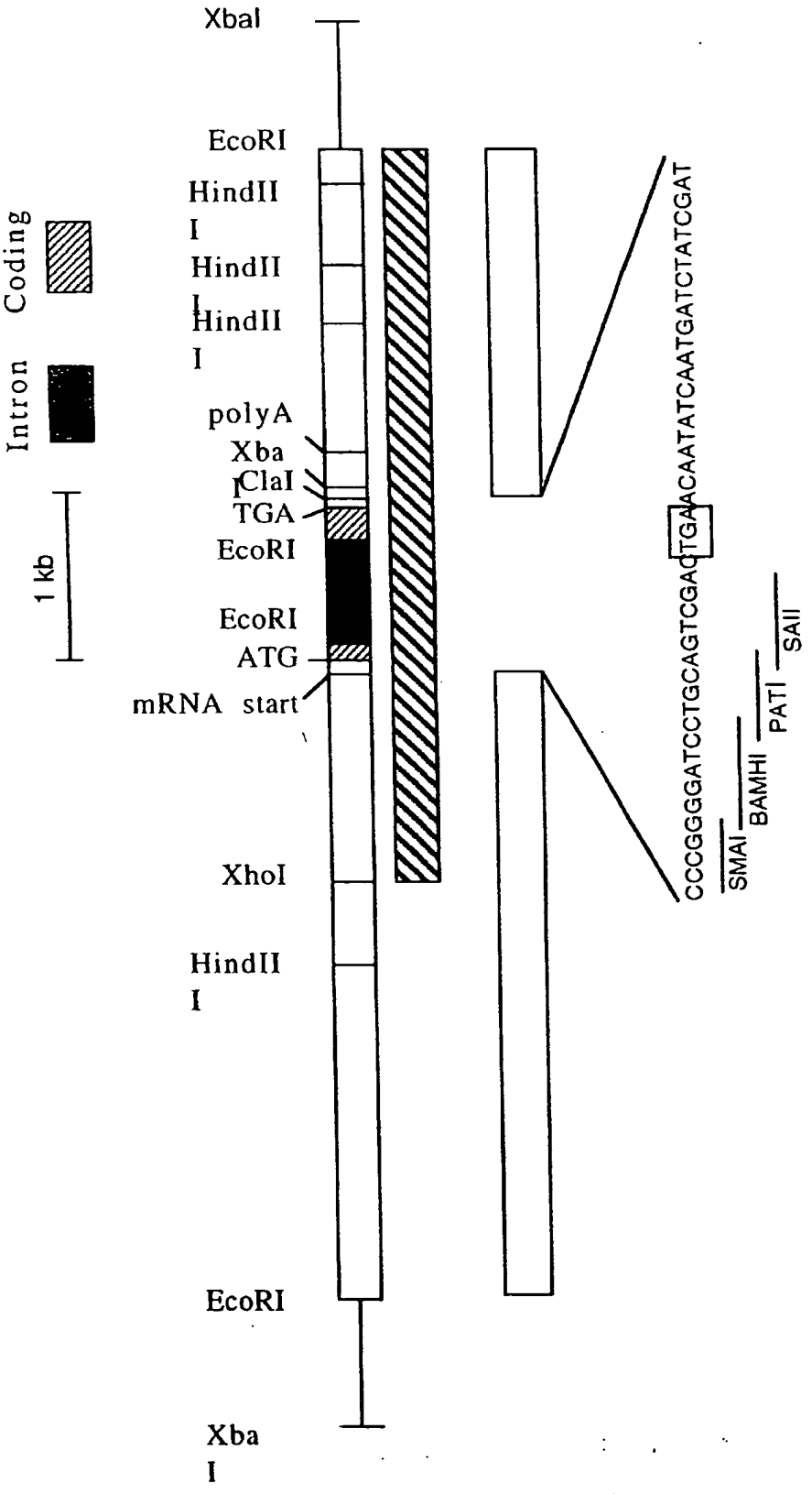
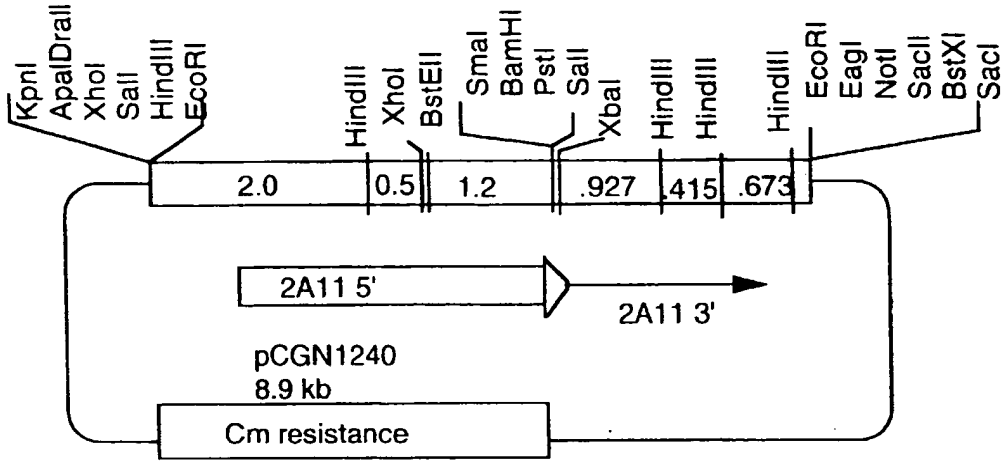


FIGURE 9



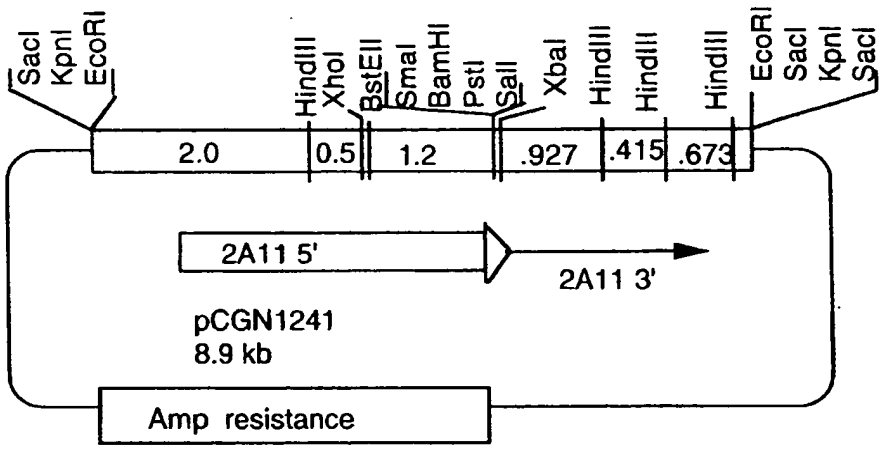
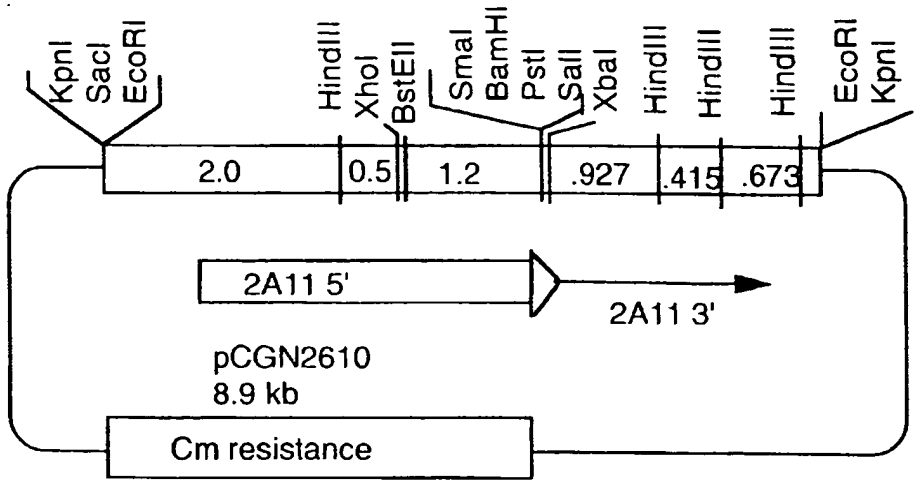


FIGURE 10A



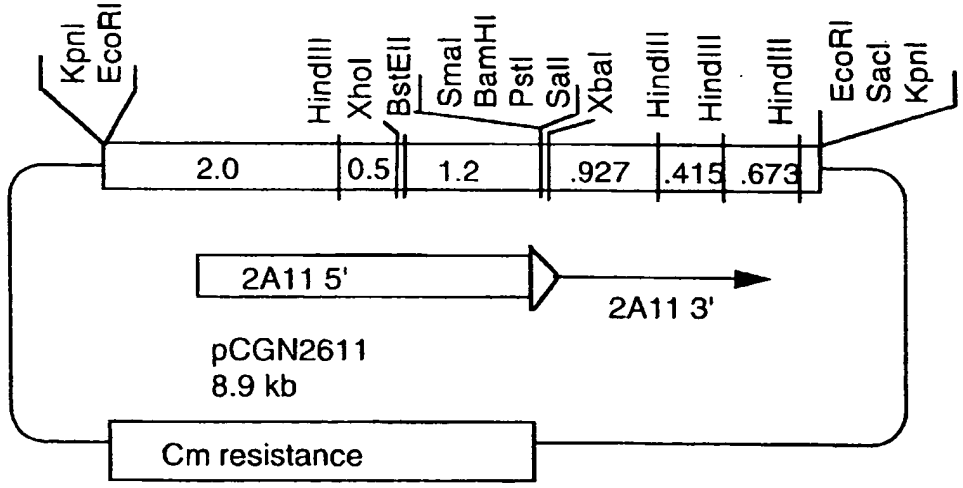


FIGURE 10B